Ex B

EC-PDB

EC 1.-.-.- EC 2.-.-.- EC 3.-.-.- EC 4.-.-.- EC 5.-.-.- EC 6.-.-.-

EC 1.6.99.3 Nadh dehydrogenase. *3 PDB entries*

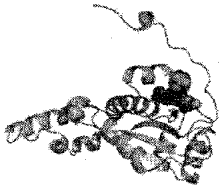
Enzymes

EC 1.-.-.- Oxidoreductases. [**3,748** PDB entries]

EC 1.6.-.- Acting on Nadh or nadph. [**122** PDB entries]

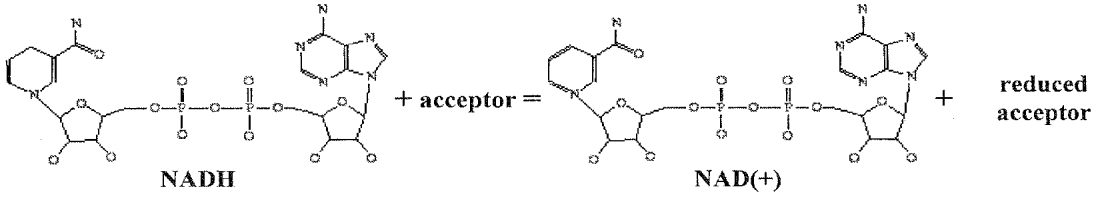
EC 1.6.99.- With other acceptors. [**17** PDB entries]

EC 1.6.99.3 **Nadh dehydrogenase.** [**3** PDB entries]



1nox

Reaction: *Nadh + acceptor = NAD(+) + reduced acceptor.*

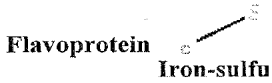


NADH NAD(+)

Molecule diagrams generated from .mol files obtained from the KEGG ftp site.

Other name(s): *Beta-Nadh dehydrogenase dinucleotide. Cytochrome c reductase. Diaphorase. Dihydrocodehydrogenase I dehydrogenase. Dihydronicotinamide adenine dinucleotide dehydrogenase. Diphosphopyrinase. Dpnh diaphorase. Nadh diaphorase. Nadh hydrogenase. Nadh oxidoreductase.*

Cofactor(s): *Flavoprotein; Iron-sulfur.*



Molecule diagrams generated from .mol files obtained from the KEGG ftp site.

Comments: *After preparations have been subjected to certain treatments cytochrome c may act as acceptor. Under normal conditions, two protons are extruded from the cytoplasm or the intramitochondrial or stromal compartment. Present in a mitochondrial complex as Ec 1.6.5.3. Formerly Ec 1.6.2.1.*

Links: [IntEnz] [ExPASy] [KEGG]

There are **3** PDB entries in enzyme class E.C.1.6.99.3

PDB code	Protein
1nox	Nadh oxidase from thermus thermophilus ***Source:*** *Thermus thermophilus. Strain: hb8. Atcc: 27634. Expressed in: escherichia coli.* ***Chain:*** *A (200 residues)* ***Bound ligand:*** *Het Group FMN is 41.00% similar to enzyme reactant NADH*
1ozk	Theoretical model for nadh-ubiquinone reductase ***Source:*** *Escherichia coli. Bacteria* ***Chain:*** *A (385 residues)* ***Bound ligand:*** *Het Group NAD corresponds to enzyme reactant NADH*
1s3a	Nmr solution structure of subunit b8 from human nadh- ubiquinone oxidoreductase complex i (ci-b8) ***Source:*** *Homo sapiens. Human. Gene: ndufa2. Expressed in: escherichia coli.* ***Chain:*** *A (85 residues)*